

- (1) contacting RNA from said sample and said control sample with a pair of primers, wherein said pair of primers consists of a first primer which hybridizes within exon 8 of the hTERT gene and a second primer which hybridizes upstream of exon 7 or downstream of exon 8 of the hTERT gene;
- (2) amplifying the nucleic acid sequence;
- (3) measuring the generation of amplification products;
- (4) determining the quantity of hTERT mRNA comprising β-region coding sequence in said sample from the results obtained in step (3); and

(b) identifying the presence of cancerous cells in said sample if the quantity of hTERT mRNA comprising β-region coding sequence in said sample is greater than the quantity of hTERT mRNA comprising β-region coding sequence in said control sample.